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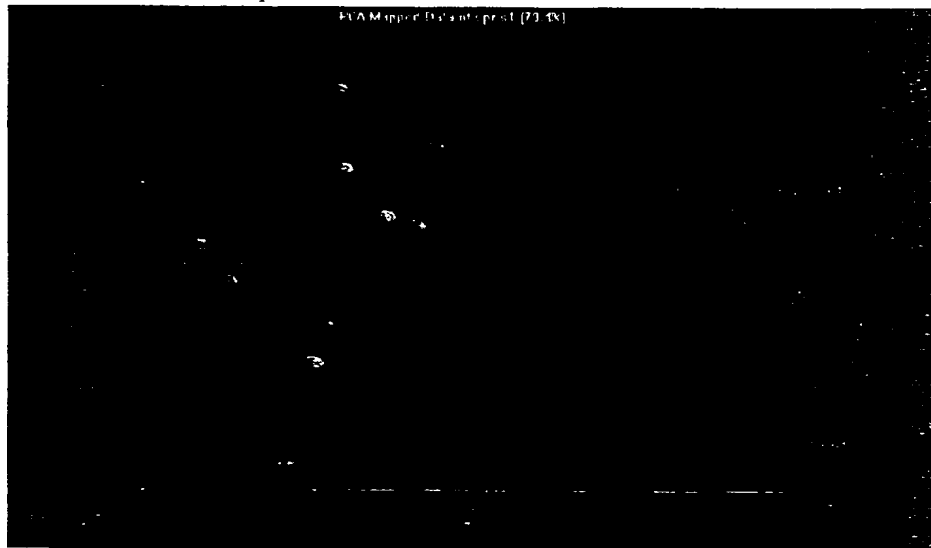
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[Continued on next page]

(54) Title: GENE EXPRESSION PROFILES IN BREAST TISSUE

- 33 Tissue Samples



(57) Abstract: The present invention results from the examination of tissue from breast carcinomas to identify genes differentially expressed between tumor biopsies and normal tissue. The invention includes diagnostic and screening methods using these genes as well as solid supports comprising oligonucleotide arrays that are complementary to or hybridize to the differentially expressed genes.

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- (c) preparing second gene expression profile of the agent-exposed cell population; and
- (d) comparing the first and second gene expression profiles.

- 5 15. The method of claim 14, wherein the breast cancer is a infiltrating ductal carcinoma.
- 16. The method of claim 14, wherein the breast cancer is a microinvasive breast cancer.
- 17. A composition comprising at least two oligonucleotides, wherein each of the
10 oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 1-5.
- 18. A composition according to claim 17, wherein the composition comprises at least 3 oligonucleotides.
- 15 19. A composition according to claim 17, wherein the composition comprises at least 5 oligonucleotides.
- 20. A composition according to claim 17, wherein the composition comprises at least 7 oligonucleotides.
- 20 21. A composition according to claim 17, wherein the composition comprises at least 10 oligonucleotides.
- 22. A composition according to any one of claims 17-21, wherein the oligonucleotides
25 are attached to a solid support.
- 23. A composition according to claim 22, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.
- 30 24. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 1-5.

25. A solid support according to claim 24, wherein the oligonucleotides are covalently attached to the solid support.
26. A solid support according to claim 24, wherein the oligonucleotides are non-
5 covalently attached to the solid support.
27. A solid support according to claim 24, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.
- 10 28. A solid support according to claim 24, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.
29. A solid support according to claim 24, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.
15
30. A solid support according to claim 24, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.
31. A computer system comprising:
20 (a) a database containing information identifying the expression level in breast tissue of a set of genes comprising at least two genes in Tables 1-5; and
(b) a user interface to view the information.
32. A computer system of claim 31, wherein the database further comprises sequence
25 information for the genes.
33. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the genes in normal breast tissue.
- 30 34. A computer system of claim 31, wherein the database further comprises information identifying the expression level for the genes in breast cancer tissue.
35. A computer system of claim 34, wherein the breast cancer tissue comprises infiltrating ductal carcinoma cells.

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* Complete entries *

ID ABT11092 standard; cDNA; 2247 BP.
 XX
 AC ABT11092;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human breast cancer associated coding sequence SEQ ID NO: 1226.
 XX
 KW Human; breast specific gene; breast cancer; differential expression;
 KW cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200259271-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US002176.
 XX
 PR 25-JAN-2001; 2001US-0263757P.
 PR 25-APR-2001; 2001US-0286090P.
 PR 23-MAY-2001; 2001US-0292517P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Orr MS, Nation M, Diggans JC, Zeng W;
 XX
 DR WPI; 2002-674803/72.
 XX
 PT Diagnosing breast cancer in a patient comprises detecting the level of
 PT gene expression in cell or tissue samples, where a differential gene
 PT expression is indicative of breast cancer.
 XX
 PS Claim 1; SEQ ID NO 1226; 260pp + Sequence Listing; English.
 XX
 CC The present invention relates to methods of diagnosing breast cancer in a
 CC patient, which comprise detecting the level of expression in a tissue
 CC sample of two or more genes selected from those shown in ABT09867-
 CC ABT11112, where a differential expression of the genes indicates breast
 CC cancer. The methods are useful in diagnosing, treating, detecting the
 CC progression, and in monitoring treatment of breast cancer in patients.
 CC The methods are also useful as a screening tool for agents that modulate
 CC the onset or progression of breast cancer. The breast cancer genes may be
 CC used as diagnostic markers for the prediction or identification of the
 CC malignant state of breast tissue, for confirming the type and progression
 CC of cancer, and for drug screening and assays. The present sequence is a
 CC coding sequence of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub.published_pct_sequences
 XX
 SQ Sequence 2247 BP; 393 A; 715 C; 675 G; 464 T; 0 U; 0 Other;
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